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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Oct 04 11:34:29 EDT 2007

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Reviewer Comments:

<210> 17

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Motif 3 (coiled coil) CORE SEQUENCE

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa can be a stretch of 1 to 6 amino acids

<220>

<221> MISC_FEATURE

<222> (4)..(5)

<223> Xaa can be any amino acid

<220>

<221> MISC_FEATURE

<222> (8)..(10)

<223> Xaa can be any amino acid

<220>

<221> MISC_FEATURE

<222> (12)..(13)

<223> Xaa can be any amino acid

<400> 17

Glu Xaa Glu Xaa Xaa Arg Leu Xaa Xaa Xaa Leu Xaa Xaa Leu Arg
1 5 10 15

The above <223> description of Xaa at location 2 is invalid: "Xaa" can only represent a single amino acid, not a stretch of amino acids. Also, which amino acid(s) does Xaa represent? Please insert 6 Xaa's, adjust the <222> response, and explain which amino acid(s) the Xaa's represent and that some may be missing. Same error in Sequence 18.

Application No: 10580085 Version No: 1.0

Input Set:

Output Set:

Started: 2007-09-20 09:17:27.983
Finished: 2007-09-20 09:17:29.893
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 910 ms
Total Warnings: 9
Total Errors: 0
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)

SEQUENCE LISTING

<110> CropDesign N.V.

<120> Seedy1 sequence for making plants having changed growth characteristics

<130> CD-105-PCT

<140> 10580085

<141> 2007-09-20

<150> US 60/528,113

<151> 2003-12-09

<150> EP 03104280.7

<151> 2003-11-19

<160> 18

<170> PatentIn version 3.3

<210> 1

<211> 1428

<212> DNA

<213> Nicotiana tabacum

<220>

<221> misc_feature

<223> seedy1 coding sequence (CDS0689)

<400> 1

atgagtgtgt tacaatacc agaagggatt gaccagcag atgttcagat atggaacaat	60
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ctgaaacccc tttcggttag gccatcagat tcctttgaat ctgatttgtc aagtaaggaa	180
aatcaaactc ctttatttga gaattcatct gttaatctct catctccgtt acccataaag	240
ccacttaacc ctaatggggc tctggaaaat tcaagactca agccgaacaa gcccaattcc	300
aaacagagtc ttgatgagat ggcggctaga aagagcggaa agggaaatga tttccgtgat	360
gagaagaaaa tagacgagga aattgaagaa attcagatgg agattagtag gttgagttca	420
agattagagg ctttgagaat tgaaaaggct gagaaaactg ttgctaagac tgttgaaaag	480
cgaggaaggg ttgtggcagc aaagtttatg gagccaaaac aaagtgttat taagattgaa	540
gagcgtatat caatgagtgc aagaacaaag gtggagcaga gaaggggtct tagtttagga	600
ccatctgaga tttttactgg aacgcggcgg cgagggttga gtatggggcc atcagatatt	660
ctagcaggga caacaaaggc acggcaattg ggaaagcaag agatgattat tactcctatt	720

cagccaatac aaaacaggcg aaagtcgtgt ttttgaagc ttcaagagat tgaagaagag 780
ggaaaaagtt caagccttag tcctaaatca agaaaaactg ctgcaagaac aatgggtaca 840
acaaggcagg cagttactac aattgcatca aagaagaatt tgaaaaaaga tgatggactt 900
ttgagttcag ttcagccaaa gaagttgttt aaagatctcg aaaagtctgc tgctgctaata 960
aagaagcccc agaggccggg gaggggtgtg gctagtaggt ataatcagag tacaattcag 1020
tcatcagtag tgagaaagag gtctttacct gaaatgata aggatgagag taagagaaat 1080
gataagaaac ggtcgttatc tgtagggaaa acgcgtgtgt ctcaaactga gagcaagaat 1140
ttgggtactg aaagtagggg gaaaaagaga tgggaaattc ctagtgagat tgtagttcat 1200
ggaaacacag agagtgagaa atctccacta agcattattg tgaagcctga tttgcttccg 1260
cgaattagga ttgctcggtg tgtgaatgag actcttaggg attctggacc tgctaaaaga 1320
atgatagagt tgataggcaa gaaatcggtt ttcagtagtg atgaagataa ggagccacct 1380
gtctgtcaag ttttaagttt tgcagaggaa gatgctgaag aggaataa 1428

<210> 2
<211> 475
<212> PRT
<213> Nicotiana tabacum

<220>
<221> MISC_FEATURE
<223> seedy1 protein (CDS0689)

<400> 2

Met Ser Val Leu Gln Tyr Pro Glu Gly Ile Asp Pro Ala Asp Val Gln
1 5 10 15

Ile Trp Asn Asn Ala Ala Phe Asp Asn Gly Asp Ser Glu Asp Leu Ser
20 25 30

Ser Leu Lys Arg Ser Trp Ser Pro Leu Lys Pro Leu Ser Val Arg Pro
35 40 45

Ser Asp Ser Phe Glu Ser Asp Leu Ser Ser Lys Glu Asn Gln Thr Pro
50 55 60

Leu Phe Glu Asn Ser Ser Val Asn Leu Ser Ser Pro Leu Pro Ile Lys
65 70 75 80

Pro Leu Asn Pro Asn Gly Ala Leu Glu Asn Ser Arg Leu Lys Pro Asn
85 90 95

Lys Pro Asn Ser Lys Gln Ser Leu Asp Glu Met Ala Ala Arg Lys Ser
100 105 110

Gly Lys Gly Asn Asp Phe Arg Asp Glu Lys Lys Ile Asp Glu Glu Ile
115 120 125

Glu Glu Ile Gln Met Glu Ile Ser Arg Leu Ser Ser Arg Leu Glu Ala
130 135 140

Leu Arg Ile Glu Lys Ala Glu Lys Thr Val Ala Lys Thr Val Glu Lys
145 150 155 160

Arg Gly Arg Val Val Ala Ala Lys Phe Met Glu Pro Lys Gln Ser Val
165 170 175

Ile Lys Ile Glu Glu Arg Ile Ser Met Ser Ala Arg Thr Lys Val Glu
180 185 190

Gln Arg Arg Gly Leu Ser Leu Gly Pro Ser Glu Ile Phe Thr Gly Thr
195 200 205

Arg Arg Arg Gly Leu Ser Met Gly Pro Ser Asp Ile Leu Ala Gly Thr
210 215 220

Thr Lys Ala Arg Gln Leu Gly Lys Gln Glu Met Ile Ile Thr Pro Ile
225 230 235 240

Gln Pro Ile Gln Asn Arg Arg Lys Ser Cys Phe Trp Lys Leu Gln Glu
245 250 255

Ile Glu Glu Glu Gly Lys Ser Ser Ser Leu Ser Pro Lys Ser Arg Lys
260 265 270

Thr Ala Ala Arg Thr Met Val Thr Thr Arg Gln Ala Val Thr Thr Ile
275 280 285

Ala Ser Lys Lys Asn Leu Lys Lys Asp Asp Gly Leu Leu Ser Ser Val
290 300

Gln Pro Lys Lys Leu Phe Lys Asp Leu Glu Lys Ser Ala Ala Ala Asn

305 310 315 320

Lys Lys Pro Gln Arg Pro Gly Arg Val Val Ala Ser Arg Tyr Asn Gln
325 330 335

Ser Thr Ile Gln Ser Ser Val Val Arg Lys Arg Ser Leu Pro Glu Asn
340 345 350

Asp Lys Asp Glu Ser Lys Arg Asn Asp Lys Lys Arg Ser Leu Ser Val
355 360 365

Gly Lys Thr Arg Val Ser Gln Thr Glu Ser Lys Asn Leu Gly Thr Glu
370 375 380

Ser Arg Val Lys Lys Arg Trp Glu Ile Pro Ser Glu Ile Val Val His
385 390 395 400

Gly Asn Thr Glu Ser Glu Lys Ser Pro Leu Ser Ile Ile Val Lys Pro
405 410 415

Asp Leu Leu Pro Arg Ile Arg Ile Ala Arg Cys Val Asn Glu Thr Leu
420 425 430

Arg Asp Ser Gly Pro Ala Lys Arg Met Ile Glu Leu Ile Gly Lys Lys
435 440 445

Ser Phe Phe Ser Ser Asp Glu Asp Lys Glu Pro Pro Val Cys Gln Val
450 455 460

Leu Ser Phe Ala Glu Glu Asp Ala Glu Glu Glu
465 470 475

<210> 3
<211> 1336
<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<223> seedy1 coding sequence

<400> 3
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ggcgacaagg agaatcaccg ccccgaggtt gttgatgtcg ccgccggcta cgacgtcgag	180
gccgagatcg gccacatcga ggcgagatc ctgcgcctct cgtcccggct ccaccatctc	240
cgcgtctcca agcagccgga gcccacccgc gacgacgtc cgatggggga gatggtcgcg	300
aaggtgaggc cccggccgag gggcctcagc ctcgggcccc tggatgtgat ctccatcgtc	360
aatcgtgaga agcatccgct gcgcaccaag cagcctccgg cgacgcgggg cagggggctc	420
agcctcgggc ccatggagat cgcgcggcg aaccctaggg tgcccgcggc ggcgagcat	480
cagcaacagc aacgcgctgg cacggcgcg atcctgaagc caatcaagga gcctccggtg	540
cagcgtcgca ggggcgtcag cctcggggcg ttggagatcc accacggcgt cggcagcaag	600
gcaccagcgg cggcgcgagc caagccgttc accaccaagc tcaacgccat tcgagaagaa	660
acccgaccct ccaagcaatt cgcgctcccc gccaagccat ggccgtcgag caatacaagg	720
cagacactgg actcgaggca aggaacagca gcaagtcgag cgaaggcgag gagcccgagc	780
cccaggccca ggaggcaatc caatggcaag gctactgaca caaggggagg caacaagggtg	840
gtggatgagc tcaagcccaa aggtgcgtcg tcaagtcaga gcggcagcgc cgcgcgcccc	900
gccactgcca agaggatggc ggggagctcc aagatgaggg tcatcccgag ccgctacagc	960
ctcactcctg gcgcttcctt tggaagcagt ggagcacagg agaggcgacg caagcagtct	1020
ctcccaggat catcagggga tgccaaccag aatgaggaaa tcagagcgaa ggtcatcgag	1080
ccttccaatg atccactctc tcctcaaacg atctccaagg ttgctgaaat gctcccaaag	1140
atcaggacca tgccgcctcc tgacgagagc cctcgcgatt ccggatgcgc caagcggggtt	1200
gccgaattgg tcgggaagcg ctcgctcttc acggctgcag ccgaggacgg gcgggcgctc	1260
gacgtcgaag cacccgaggc ggtcgcagaa gcttgagatg aaccaccatg gtttgatccg	1320
ttccttccat cagctc	1336

<210> 4
 <211> 431
 <212> PRT
 <213> Oryza sativa

<220>
 <221> MISC_FEATURE
 <223> seedy1 protein

<400> 4

Met Glu Glu Asp Pro Leu Ile Pro Leu Val His Val Trp Asn Asn Ala

1	5	10	15
Ala Phe Asp Asp Ser Ser Cys Ser Arg Ser Ala Trp Leu Pro Gln Ser	20	25	30
Pro Ala Val Ala Ala Val Arg Lys Gly Asp Lys Glu Asn His Arg Pro	35	40	45
Glu Val Val Asp Val Ala Ala Gly Tyr Asp Val Glu Ala Glu Ile Gly	50	55	60
His Ile Glu Ala Glu Ile Leu Arg Leu Ser Ser Arg Leu His His Leu	65	70	75
Arg Val Ser Lys Gln Pro Glu Pro Asn Arg Asp Asp Ala Pro Met Gly	85	90	95
Glu Met Val Ala Lys Val Arg Pro Arg Pro Arg Gly Leu Ser Leu Gly	100	105	110
Pro Leu Asp Val Ile Ser Ile Val Asn Arg Glu Lys His Pro Leu Arg	115	120	125
Thr Lys Gln Pro Pro Ala Thr Arg Gly Arg Gly Leu Ser Leu Gly Pro	130	135	140
Met Glu Ile Ala Ala Ala Asn Pro Arg Val Pro Ala Ala Ala Gln His	145	150	155
Gln Gln Gln Gln Arg Ala Gly Thr Ala Arg Ile Leu Lys Pro Ile Lys	165	170	175
Glu Pro Pro Val Gln Arg Arg Arg Gly Val Ser Leu Gly Pro Leu Glu	180	185	190
Ile His His Gly Val Gly Ser Lys Ala Pro Ala Ala Ala Arg Ala Lys	195	200	205
Pro Phe Thr Thr Lys Leu Asn Ala Ile Arg Glu Glu Thr Arg Pro Ser	210	215	220
Lys Gln Phe Ala Val Pro Ala Lys Pro Trp Pro Ser Ser Asn Thr Arg	225	230	235
			240

Gln Thr Leu Asp Ser Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala
245 250 255

Arg Ser Pro Ser Pro Arg Pro Arg Arg Gln Ser Asn Gly Lys Ala Thr
260 265 270

Asp Thr Arg Gly Gly Asn Lys Val Val Asp Glu Leu Lys Pro Lys Gly
275 280 285

Ala Ser Ser Ser Gln Ser Gly Ser Ala Ala Ala Ala Ala Thr Ala Lys
290 295 300

Arg Met Ala Gly Ser Ser Lys Met Arg Val Ile Pro Ser Arg Tyr Ser
305 310 315 320

Leu Thr Pro Gly Ala Ser Leu Gly Ser Ser Gly Ala Gln Glu Arg Arg
325 330 335

Arg Lys Gln Ser Leu Pro Gly Ser Ser Gly Asp Ala Asn Gln Asn Glu
340 345 350

Glu Ile Arg Ala Lys Val Ile Glu Pro Ser Asn Asp Pro Leu Ser Pro
355 360 365

Gln Thr Ile Ser Lys Val Ala Glu Met Leu Pro Lys Ile Arg Thr Met
370 375 380

Pro Pro Pro Asp Glu Ser Pro Arg Asp Ser Gly Cys Ala Lys Arg Val
385 390 395 400

Ala Glu Leu Val Gly Lys Arg Ser Phe Phe Thr Ala Ala Ala Glu Asp
405 410 415

Gly Arg Ala Leu Asp Val Glu Ala Pro Glu Ala Val Ala Glu Ala
420 425 430

<210> 5

<211> 1860

<212> DNA

<213> *Medicago trunculata*

<220>

<221> misc_feature
<223> seedy1 coding sequence

<400> 5

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cctatttaca gggatcttaa atataattaa ccctaattatt tatgacagaa acccttttga	120
aatcacatcg gagcgtgtat gagtagccgt ttcacatcca acggccagta agagcgtaac	180
tttatttctt ccctcttcaa tctccaacgg tcacataatc tcttccaaat acaaataatt	240
ccctctttca acctcactct tcattttctt aacccaaacc caaaaaacta atcagattct	300
tcttaaattct tgaaaccttt ctcccaaaag cacttaaata aaaaagcact taacctgaa	360
taacacaaac aacaacaaca ttcttcttca ttccacacag gttcaagtgt ggaacaacgc	420
agcattcgat ggtgaagatt tcgccatgaa ttcatcttct gattccatca aagagaatct	480
aaacccatcc gcattcaaca ttgttccttc ttcaaacaaa agaactattg atgatgaaat	540
tgcggaattt gaaagtgaat ttaagcgatt aacttcgaag ctggaattgc ttcgtgttga	600
aaaagctgaa agaaaaatcg cttctgaaaa gcgtgttagt ggaatttggt ctggaagaat	660
agtagcagcg aagtttatgg aaccgaagaa aaacgttaca ccgaaacgaa acggtgtcgt	720
tttcaaggag gagacaccga aacgaaacgg tgctgtttcg gatacgccga aatctagggt	780
taattggaga agagggatga gtttaggtcc gatggagatt gccgggaaag tgatggcacc	840
gccggcgatg acgattactc cggcgacggg gaatcgaggg aagtcttgtt tctggaaacc	900
gcaggaaagt tgtgaagtaa tgccgtcggg gattactccg gcgacggtga ataggaggaa	960
atcttgtttt ttgaaacctc aagaaagttg tgaagaaaat cgaagaaaaa cgatttgcaa	1020
accgaatttg aatttgaatt caaattcagt taattctgcg gttggatcga ttaagcgtgt	1080
gaagaagaaa gatgaagaaa ttgctcaggt tcaaccgaag aagctgtttg aaggtgaaaa	1140
atcagtgaag aaatcggtga aacaaggtag aattgttgca agccgtata attccggtgg	1200
tggtggtggt gatgcgagga aaagatcggt ttcggagaat aataagggtt tagggagtga	1260
aatcagggct aagaagagat gggagatacc aattgaagaa gtggatgtga gtggttttgt	1320
tatgttaccg aagatttcga caatgaggtt tggtgatgag agtcctagag attctggtgc	1380
tggttaaaaga gttgctgaat tgaatggaaa aagatcttac ttttgtgatg aagatgagga	1440
ggagagagtg atggtggagg aagaagggtg ttctgtttgt cagggttttga attttgctga	1500
agatgatgat gatgatgatg attatggtga acaagggtaa ttgtggaaat tggaattgat	1560
ttgtttttgt ggggttgtgt ggaactggct atgttctgct tgattctttt gcatttttgt	1620

gtgaaactaa agatgagggtg aaaagtttat gcttggttaa ttggattggt ttatatgttt 1680
 tgaaataata acaacaagca tgtgtcttgc ttaataattg tatattgttt tgtttgtttt 1740
 ataatgatat ggatttaatt tgtatacaca atataatata gtatgcattg agagagtttt 1800
 tcgttcagta ttcattctga ttttagtggt tatctcattc tagaagattg tattttgttg 1860

<210> 6
 <211> 394
 <212> PRT
 <213> Medicago trunculata

<220>
 <221> MISC_FEATURE
 <223> seedy1 protein

<400> 6

Met Asn Asn Thr Asn Asn Asn Asn Ile Leu Leu His Ser Thr Gln Val
 1 5 10 15

Gln Val Trp Asn Asn Ala Ala Phe Asp Gly Glu Asp Phe Ala Met Asn
 20 25 30

Ser Ser Ser Asp Ser Ile Lys Glu Asn Leu Asn Pro Ser Ala Phe Asn
 35 40 45

Ile Val Pro Ser Ser Asn Lys Arg Thr Ile Asp Asp Glu Ile Ala Glu
 50 55 60

Ile Glu Ser Glu Ile Lys Arg Leu Thr Ser Lys Leu Glu Leu Leu Arg
 65 70 75 80

Val Glu Lys Ala Glu Arg Lys Ile Ala Ser Glu Lys Arg Val Ser Gly
 85 90 95

Ile Gly Thr Gly Arg Ile Val Ala Ala Lys Phe Met Glu Pro Lys Lys
 100 105 110

Asn Val Thr Pro Lys Arg Asn Gly Val Val Phe Lys Glu Glu Thr Pro
 115 120 125

Lys Arg Asn Gly Val Val Ser Asp Thr Pro Lys Ser Arg Val Asn Trp
 130 135 140

Arg Arg Gly Met Ser Leu Gly Pro Met Glu Ile Ala Gly Lys Val Met
145 150 155 160

Ala Pro Pro Ala Met Thr Ile Thr Pro Ala Thr Val Asn Arg Arg Lys
165 170 175

Ser Cys Phe Trp Lys Pro Gln Glu Ser Cys Glu Val Met Pro Ser Gly
180 185 190

Ile Thr Pro Ala Thr Val Asn Arg Arg Lys Ser Cys Phe Leu Lys Pro
195 200 205

Gln Glu Ser Cys Glu Glu Asn Arg Arg Lys Thr Ile Cys Lys Pro Asn
210 215 220

Leu Asn Leu Asn Ser Asn Ser Val Asn Ser Ala Val Gly Ser Ile Lys
225 230 235 240

Arg Val Lys Lys Lys Asp Glu Glu Ile Ala Gln Val Gln Pro Lys Lys
245 250 255

Leu Phe Glu Gly Glu Lys Ser Val Lys Lys Ser Leu Lys Gln Gly Arg
260 265 270

Ile Val Ala Ser Arg Tyr Asn Ser Gly Gly Gly Gly Gly Asp Ala Arg
275 280 285

Lys Arg Ser Phe Ser Glu Asn Asn Lys Gly Leu Gly Ser Glu Ile Arg
290 295 300

Ala Lys Lys Arg Trp Glu Ile Pro Ile Glu Glu Val Asp Val Ser Gly
305 310 315 320

Phe Val Met Leu Pro Lys Ile Ser Thr Met Arg Phe Val Asp Glu Ser
325 330 335

Pro Arg Asp Ser Gly Ala Val Lys Arg Val Ala Glu Leu Asn Gly Lys
340 345